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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=12; day=4; hr=7; min=24; sec=12; ms=815;]

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Application No: 09540245 Version No: 1.0

Input Set:

Output Set:

Started: 2008-12-02 10:18:59.302
Finished: 2008-12-02 10:19:02.950
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 648 ms
Total Warnings: 14
Total Errors: 1
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
E 341	'Xaa' position not defined SEQID (5) POS (153)
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W 402	Undefined organism found in <213> in SEQ ID (19)
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<110> APPLICANT: Goodman, Corey

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Brose, Katja

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<120> TITLE OF INVENTION: Modulating Robo: Ligand Interactions

<130> FILE REFERENCE: B98-031-3

<140> CURRENT APPLICATION NUMBER: 09540245

<141> CURRENT FILING DATE: 2000-03-31

<150> PRIOR APPLICATION NUMBER: 60/065,544

<151> PRIOR FILING DATE: 1997-11-14

<150> PRIOR APPLICATION NUMBER: 60/081,057

<151> PRIOR FILING DATE: 1998-04-07

<160> NUMBER OF SEQ ID NOS: 20

<170> SOFTWARE: PatentIn Ver. 2.0

<210> SEQ ID NO 1

<211> LENGTH: 4758

<212> TYPE: DNA

<213> ORGANISM: human

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(4575)

<400> SEQUENCE: 1

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1			5					10						15		
ctg	gcg	atc	ctg	aac	aag	gtg	gca	ccg	cag	gcg	tgc	ccg	gcg	cag	tgc	96
Leu	Ala	Ile	Leu	Asn	Lys	Val	Ala	Pro	Gln	Ala	Cys	Pro	Ala	Gln	Cys	
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tct	tgc	tcg	ggc	agc	aca	gtg	gac	tgt	cac	ggg	ctg	gcg	ctg	cgc	agc	144
Ser	Cys	Ser	Gly	Ser	Thr	Val	Asp	Cys	His	Gly	Leu	Ala	Leu	Arg	Ser	
			35				40					45				
gtg	ccc	agg	aat	atc	ccc	cgc	aac	acc	gag	aga	ctg	gat	tta	aat	gga	192
Val	Pro	Arg	Asn	Ile	Pro	Arg	Asn	Thr	Glu	Arg	Leu	Asp	Leu	Asn	Gly	
			50				55				60					
aat	aac	atc	aca	aga	att	acg	aag	aca	gat	ttt	gct	ggt	ctt	aga	cat	240
Asn	Asn	Ile	Thr	Arg	Ile	Thr	Lys	Thr	Asp	Phe	Ala	Gly	Leu	Arg	His	
			65				70			75			80			
cta	aga	gtt	ctt	cag	ctt	atg	gag	aat	aag	att	agc	acc	att	gaa	aga	288
Leu	Arg	Val	Leu	Gln	Leu	Met	Glu	Asn	Lys	Ile	Ser	Thr	Ile	Glu	Arg	
			85				90					95				
gga	gca	ttc	cag	gat	ctt	aaa	gaa	cta	gag	aga	ctg	cgt	tta	aac	aga	336
Gly	Ala	Phe	Gln	Asp	Leu	Lys	Glu	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Arg	
			100				105				110					
aat	cac	ctt	cag	ctg	ttt	cct	gag	ttg	ctg	ttt	ctt	ggg	act	gcg	aag	384
Asn	His	Leu	Gln	Leu	Phe	Pro	Glu	Leu	Phe	Leu	Gly	Thr	Ala	Lys		
			115				120			125						
cta	tac	agg	ctt	gat	ctc	agt	gaa	aac	caa	att	cag	gca	atc	cca	agg	432
Leu	Tyr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Ala	Ile	Pro	Arg	
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Lys	Ala	Phe	Arg	Gly	Ala	Val	Asp	Ile	Lys	Asn	Leu	Gln	Leu	Asp	Tyr	
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aac	cag	atc	agc	tgt	att	gaa	gat	ggg	gca	ttc	agg	gct	ctc	cgg	gac	528
Asn	Gln	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu	Arg	Asp	
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gca agt ttc aac cat atg cct aaa ctt agg act ttt cga ctg cat tca	624
Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser	
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aac aac ctg tat tgt gac tgc cac ctg gcc tgg ctc tcc gac tgg ctt	672
Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu	
210 215 220	
cgc aaa agg cct cgg gtt ggt ctg tac act cag tgt atg ggc ccc tcc	720
Arg Lys Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser	
225 230 235 240	
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His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val	
245 250 255	
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Cys Ser Asp Glu Glu Gly His Gln Ser Phe Met Ala Pro Ser Cys	
260 265 270	
agt gtt ttg cac tgc cct gcc gcc tgt acc tgt agc aac aat atc gta	864
Ser Val Leu His Cys Pro Ala Ala Cys Thr Cys Ser Asn Asn Ile Val	
275 280 285	
gac tgt cgt ggg aaa ggt ctc act gag atc ccc aca aat ctt cca gag	912
Asp Cys Arg Gly Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu	
290 295 300	
acc atc aca gaa ata cgt ttg gaa cag aac aca atc aaa gtc atc cct	960
Thr Ile Thr Glu Ile Arg Leu Glu Gln Asn Thr Ile Lys Val Ile Pro	
305 310 315 320	
cct gga gct ttc tca cca tat aaa aag ctt aga cga att gac ctg agc	1008
Pro Gly Ala Phe Ser Pro Tyr Lys Lys Leu Arg Arg Ile Asp Leu Ser	
325 330 335	
aat aat cag atc tct gaa ctt gca cca gat gct ttc caa gga cta cgc	1056
Asn Asn Gln Ile Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg	
340 345 350	
tct ctg aat tca ctt gtc ctc tat gga aat aaa atc aca gaa ctc ccc	1104
Ser Leu Asn Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro	
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Lys Ser Leu Phe Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Asn	
370 375 380	
gcc aac aag ata aac tgc ctt cgg gta gat gct ttt cag gat ctc cac	1200
Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His	
385 390 395 400	
aac ttg aac ctt ctc tcc cta tat gac aac aag ctt cag acc atc gcc	1248
Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala	
405 410 415	
aag ggg acc ttt tca cct ctt cgg gcc att caa act atg cat ttg gcc	1296
Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala	
420 425 430	
cag aac ccc ttt att tgt gac tgc cat ctc aag tgg cta gcg gat tat	1344
Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr	
435 440 445	
ctc cat acc aac ccg att gag acc agt ggt gcc cgt tgc acc agc ccc	1392
Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro	
450 455 460	
cgc cgc ctg gca aac aaa aga att gga cag atc aaa agc aag aaa ttc	1440
Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe	
465 470 475 480	

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Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys	
485 490 495	
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Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr	
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Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro	
515 520 525	
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Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu	
530 535 540	
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Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu Arg Lys Ile Asn	
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Phe Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly Ala Phe Glu Gly	
565 570 575	
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Ala Ser Gly Val Asn Glu Ile Leu Thr Ser Asn Arg Leu Glu Asn	
580 585 590	
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595 600 605	
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Leu Arg Ser Asn Arg Ile Thr Cys Val Gly Asn Asp Ser Phe Ile Gly	
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ctc agt tct gtg cgt ttg ctt tct ttg tat gat aat caa att act aca	1920
Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Gln Ile Thr Thr	
625 630 635 640	
gtt gca cca ggg gca ttt gat act ctc cat tct tta tct act cta aac	1968
Val Ala Pro Gly Ala Phe Asp Thr Leu His Ser Leu Ser Thr Leu Asn	
645 650 655	
ctc ttg gcc aat cct ttt aac tgt aac tgc tac ctg gct tgg ttg gga	2016
Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys Tyr Leu Ala Trp Leu Gly	
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Glu Trp Leu Arg Lys Lys Arg Ile Val Thr Gly Asn Pro Arg Cys Gln	
675 680 685	
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Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala Ile Gln	
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Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser Cys Ser Pro Leu	
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tct cgc tgt cct act gaa tgt act tgc ttg gat aca gtc gtc cga tgt	2208
Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys	
725 730 735	
agc aac aag ggt ttg aag gtc ttg ccg aaa ggt att cca aga gat gtc	2256
Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val	
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aca gag ttg tat ctg gat gga aac caa ttt aca ctg gtt ccc aag gaa	2304
Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu	
755 760 765	
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Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg	
770 775 780	

ata agc acg ctt tct aat cag agc ttc agc aac atg acc cag ctc ctc	2400
Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu	
785 790 795 800	
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Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr	
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Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp	
820 825 830	
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Ile Ser Val Val Pro Glu Gly Ala Phe Asn Asp Leu Ser Ala Leu Ser	
835 840 845	
cat cta gca att gga gcc aac cct ctt tac tgt gat tgt aac atg cag	2592
His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln	
850 855 860	
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Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala	
865 870 875 880	
cgt tgt gct ggt cct gga gaa atg gca gat aaa ctt tta ctc aca act	2688
Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Thr Thr	
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ccc tcc aaa aaa ttt acc tgt caa ggt cct gtg gat gtc aat att cta	2736
Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp Val Asn Ile Leu	
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gct aag tgt aac ccc tgc cta tca aat ccg tgt aaa aat gat ggc aca	2784
Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr	
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